```
                                        H   S   P   S   P   T   A   L   F   C   L      11
GGAGTCGACCCACGCGTCCGCAGGGGCTGAGGAACC ATG TCT CCA TCC CCG ACC GCC CTC TTC TGT CTT      68

  G   L   C   L   G   R   V   P   A   Q   S   G   P   L   P   K   P   S   L   Q      31
GGG CTG TGT CTG GGG CGT GTG CCA GCG CAG AGT GGA CCG CTC CCC AAG CCC TCC CTC CAG      128

  A   L   P   S   S   L   V   P   L   E   K   P   V   T   L   R   C   Q   G   P      51
GCT CTG CCC AGC TCC CTG GTG CCC CTG GAG AAG CCA GTG ACC CTC CGG TGC CAG GGA CCT      188

  P   G   V   D   L   Y   R   L   E   K   L   S   S   S   R   Y   Q   D   Q   A      71
CCG GGC GTG GAC CTG TAC CGC CTG GAG AAG CTG AGT TCC AGC AGG TAC CAG GAT CAG GCA      248

  V   L   F   I   P   A   H   K   R   S   L   A   G   R   Y   R   C   S   Y   Q      91
GTC CTC TTC ATC CCG GCC ATG AAG AGA AGT CTG GCT GGA CGC TAC CGG TGC TCC TAC CAG      308

  N   G   S   L   W   S   L   P   S   D   Q   L   E   L   V   A   T   G   V   F      111
AAC GGA AGC CTC TGG TCC CTG CCC AGC GAC CAG CTG GAG CTC GTT GCC ACG GGA GTT TTT      368

  A   K   P   S   L   S   A   Q   P   G   P   A   V   S   S   G   G   D   V   T      131
GCC AAA CCC TCG CTC TCA GCC CAG CCC GGC CCG GCG GTG TCG TCA GGA GGG GAC GTA ACC      428

  L   Q   C   Q   T   R   Y   G   F   D   Q   F   A   L   Y   K   E   G   D   P      151
CTA CAG TGT CAG ACT CGG TAT GGC TTT GAC CAA TTT GCT CTG TAC AAG GAA GGG GAC CCT      488

  A   P   Y   K   N   P   E   R   W   Y   R   A   S   F   P   I   I   T   V   T      171
GCG CCC TAC AAG AAT CCC GAG AGA TGG TAC CGG GCT AGT TTC CCC ATC ATC ACG GTG ACC      548

  A   A   H   S   G   T   Y   R   C   Y   S   F   S   S   R   D   P   Y   L   W      191
GCC GCC CAC AGC GGA ACC TAC CGA TGC TAC AGC TTC TCC AGC AGG GAC CCA TAC CTG TGG      608

  S   A   P   S   D   P   L   E   L   V   V   T   G   T   S   V   T   P   S   R      211
TCG GCC CCC AGC GAC CCC CTG GAG CTT GTG GTC ACA GGA ACC TCT GTG ACC CCC AGC CGG      668

  L   P   T   E   P   P   S   S   V   A   E   F   S   E   A   T   A   E   L   T      231
TTA CCA ACA GAA CCA CCT TCC TCG GTA GCA GAA TTC TCA GAA GCC ACC GCT GAA CTG ACC      728

  V   S   F   T   N   K   V   F   T   T   E   T   S   R   S   I   T   T   S   P      251
GTC TCA TTC ACA AAC AAA GTC TTC ACA ACT GAG ACT TCT AGG AGT ATC ACC ACC AGT CCA      788

  K   E   S   D   S   P   A   G   P   A   R   Q   Y   Y   T   K   G   N   L   V      271
AAG GAG TCA GAC TCT CCA GCT GGT CCT GCC CGC CAG TAC TAC ACC AAG GGC AAC CTG GTC      848

  R   I   C   L   G   A   V   I   L   I   I   L   A   G   F   L   A   E   D   W      291
CGG ATA TGC CTC GGG GCT GTG ATC CTA ATA ATC CTG GCG GGG TTT CTG GCA GAG GAC TGG      908

  H   S   R   R   K   R   L   R   H   R   G   R   A   V   Q   R   P   L   P   P      311
CAC AGC CGG AGG AAG CGC CTG CGG CAC AGG GGC AGG GCT GTG CAG AGG CCG CTT CCG CCC      968

  L   P   P   L   P   Q   T   R   K   S   H   G   G   Q   D   G   G   R   Q   D      331
CTG CCG CCC CTC CCG CAG ACC CGG AAA TCA CAC GGG GGT CAG GAT GGA GGC CGA CAG GAT      1028

  V   H   S   R   G   L   C   S   *                                                 340
GTT CAC AGC CGC GGG TTA TGT TCA TGA                                                1055
```
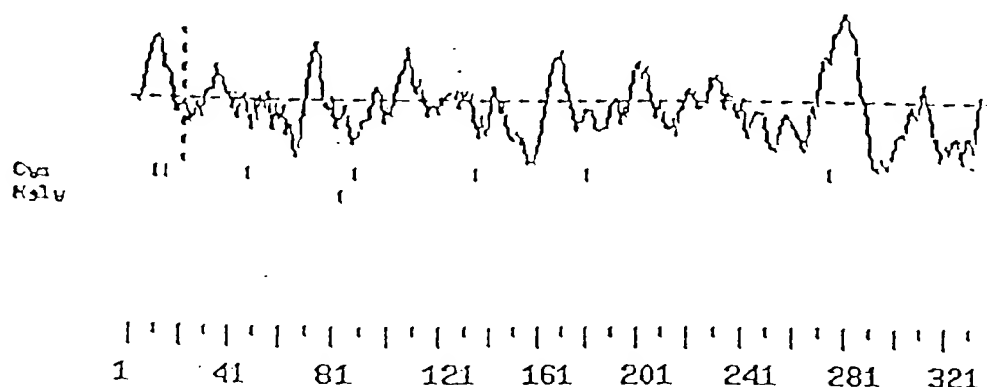
FIGURE 1a

CCGCTGAACCCCAGGCACGGTCGTATCCAAGGGAGGGATCATGGCATGGGAGGCGACTCAAAGACTGGCGTGTGTGGAG 1134

CGTGGAAGCAGGAGGGCAGAGGCTACAGCTGTGGAAACGAGGCCATGCTGCCTCCTCCTGGTGTTCCATCAGGGAGCCG 1213

TTCGGCCAGTGTCTGTCTGTCTGTCTGCCTCTCTGTCTGAGGGCACCCTCCATTTGGGATGGAAGGAATCTGTGGAGAC 1292

CCCATCCTCCTCCCTGCACACTGTGGATGACATGGTACCCTGGCTGGACCACATACTGGCCTCTTTCTTCAACCTCTCT 1371

AATATGGGCTCCAGACGGATCTCTAAGGTTCCCAGCTCTCAGGGTTGACTCTGTTCCATCCTCTGTGCAAAATCCTCCT 1450

GTGCTTCCCTTTGGCCCTCTGTGCTCTTGTCTGGTTTTCCCCAGAAACTCTCACCCTCACTCCATCTCCCACTGCGGTC 1529

TAACAAATCTCCTTTCGTCTCTCAGAACGGGTCTTGCAGGCAGTTTGGGTATGTCATTCATTTTCCTTAGTGTAAAACT 1608

AGCACGTTGCCCGCTTCCCTTCACATTAGAAAACAAGATCAGCCTGTGCAACATGGTGAAACCTCATCTCTACCAACAA 1687

AACAAAAAAACACAAAAATTAGCCAGGTGTGGTGGTGCATCCCTATACTCCCAGCAACTCGGGGGGCTGAGGTGGGAGA 1766

ATGGCTTGAGCCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATCACACCACTGCACTCTAGCTCGGGTGACGAAGCCTGA 1845

CCTTGTCTCAAAAAATACAGGGATGAATATGTCAATTACCCTGATTTGATCATAGCACGTTGTATACATGTACTGCAAT 1924

ATTGCTGTCCACCCCATAAATATGTACAATTATGTATACATTTTTAAAATCATAAAAATAAGATAATGAAAAAAAAAAA 2003

AAAAAAAAAAAAAGGGCGGGCCGCTAGACTAGTCTAGAGAACA 2047

FIGURE 1b

Cys
Kslv

```
 I ' I ' I ' I ' I ' I ' I ' I ' I ' I ' I ' I ' I ' I ' I ' I ' I ' I '
  1    41    81    121   161   201   241   281   321
```

HSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLE
KLSSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP
GPAVSSGGDVTLQCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPIITVTAAHSGTYRC
YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT
TETSRSITTSPKESDSPAGPARQYYTKGNLVRICLGAVILIILAGFLAEDWHSRRKRLRH
RGRAVQRPLPPLPPLPQTRKSHGGQDGGRQDVHSRGLCS

FIGURE 2

```
ALIGN calculates a global alignment of two sequences
  version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> U91928 ORF
> hT268 ORF                                      1893 aa vs.
scoring matrix: pam120.mat, gap penalties: -12/-4   1017 aa
37.7% identity;          Global alignment score: -8

              10        20        30        40        50        60        70
inputs ATGACGCCCGCCCTCACAGCCCTGCTCTGCCTTGGGCTGAGTCTGGGCCCCAGGACCCGCGTGCAGGCAG
       ::.:.: ::  ::: :: ::::: :::: :::::::::.:::::: :  .: .:: :: ::::: .:
       ATGTCTCCATCCCCGACCGCCCTCTTCTGTCTTGGGCTGTGTCTGGGGCG-TGTGCCAGC--GCAGAGTG
            10        20        30        40        50        60

              80        90       100       110       120       130
inputs GGCCCTTCCCCAAACCCACCCTCTGGGCTGAGCCAGGCTCTGTGAT-CAGCTGGGGGAGCCCCGTGACCA
       :.:: ::::::::.::.:.::::: .:::: .::: .::::  ::..: : :::::.:.:::: ::::::
       GACCGCTCCCCAAGCCCTCCCTCCAGGCTCTGCCCAGCTCCCTGGTGCCCCTGGAGAAGCCA-GTGACCC
            70        80        90       100       110       120       130

       140       150       160       170       180       190       200
inputs TCTGGTGTCAGGGGAGCCTGGAGGCCCAGGAGTACCGACTGGATAAAGAGGGAAGCCCAGAGCCCTTGGA
       ::  ::::: ::::: .:::   ::..:: ::. ::: :..        ::: .:::        ...
       TCCGGTGCCAGGG--ACCT------CCGGGCGTG--GACCTGTA--------CCGCCTGGAG-----AAG
            140       150            160     170                 180

       210      '220       230       240       250       260       270
inputs CAGAAATAACCCACTGGAACCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCG
       :.::..: ::  .:.::::.::::: ::: .   ::: ::::::::. ::::::: .... . :. ::
       CTGAGTT--CCAGCAGGTACC-AGGATCA-GGCAGTCCTCTTCATCCCGGCCATGAAGAGAAGTCTGGCT
            190       200       210       220       230       240

       280       290       300       310       320       330       340
inputs GGGAGATACCGCTGCCACTATTACAGCTCTGCAG--GCTGGTCAGAGCCCAGCGACCCCCTGGAGCTGGT
       ::. : :::::::::: ::: ::: .: : :: ::::::  .:::::::::::. :::::::: ::
       GGACGCTACCGCTGCTCCTAC--CAGAACGGAAGCCTCTGGTCCCTGCCCAGCGACCAGCTGGAGCTCGT
            250       260       270       280       290       300       310

       350       360       370       380       390       400       410
inputs GATGACAGGATTCTACAACAAACCCACCCTCTCAGCCCTGCCCAGCCCTGTGGTGGCCTCAGGGGGGAAT
       .   :!.::: : :. - ::::::::.: :::::::::::.::::.:::: : :::: :.::::.:::.:
       TGCCACGGGAGTTTTTGCCAAACCCTCGCTCTCAGCCCAGCCCGGCCCGGCGGTGTCGTCAGGAGGGGAC
            320       330       340       350       360       370       380

       420       430       440       450       460       470       480
inputs ATGACCCTCCGATGTGGCTCACAGAAGGGATATCACCATTTTGTTCTGATGAAGGAAGGAGAACACCAGC
       .:.:::::: :..:::  .:.:.:.: ::.:.: :.: :::::.:::: :::::.. ::::::::
       GTAACCCTACAGTGTCAGACTCGGTATGGCTTTGACCAATTTGCTCTGTACAAGGAAGG-----------
            390       400       410       420       430       440

       490      . 500       510       520       530       540       550
inputs TCCCCCGGACCCTGGACTCACAGCAGCTCCACAGTGGGGGGGTTCCAGGCCCTGTTCCCTGTGGGCCCCGT
       ::::::::                               :  ::::::.           :..
```

FIGURE 3a

```
      ------GGACCCTG-----------------------------------C---GCCCTA--------------CAA
            450                                              460

       560       570       580       590       600       610       620
inputs GAACCCCAGCCACAGGTGGAGGTTCACATGCTATTACTATTATATGAACACCCCCCAGGTGTGGTCCCAC
       ::: :::...        :.:..:::.: :. :::: :    ::        ::::          ::
       GAATCCCGA------GAGATGGTAC-CGGGCTAGT----TT----------CCCCAT--------CAT
        470               480       490                        500

       630       640       650       660       670       680       690
inputs CCCAGTGACCCCCTGGAGATTCTGCCCTCAGGCGTGTCTAGGAAGCCCTCCCTCCTGACCCTGCAGGGCC
       : :.:::::: ::          ::::.:::
       CACGGTGACCGCC----------GCCCACAG-----------------------------------
        510               520

       700       710       720       730       740       750       760
inputs CTGTCCTGGCCCCTGGGCAGAGCCTGACCCTCCAGTGTGGCTCTGATGTCGGCTACGACAGATTTGTTCT
          :.::.:::.      ::..::                ::::..:        ::::
       ----------------CGGAACCTA-----CCGATG---------------CTACAGC-------TTCT
                        530       540                        540         550

       770       780       790       800       810       820       830
inputs GTATAAGGAGGGGGAACGTGACTTCCTCCAGCGCCCTGGCCAGCAGCCCCAGGCTGGGCTCTCCCAGGCC
                                            :::::::
       ------------------------------------CCAGCAG--------------------------

       840       850       860       870       880       890       900
inputs AACTTCACCCTGGGCCCTGTGAGCCCCTCCCACGGGGGCCAGTACAGGTGCTATGGTGCACACAACCTCT
                ::.:::.                                              .::::
       ----------GGACCCA--------------------------------------------TACCT--
                560

       910       920       930       940       950       960       970
inputs CCTCCGAGTGGTCGGCCCCCAGCGACCCCCTGAACATCCTGATGGCAGGACAGATCTATGACACCGTCTC
            :::::::::::::::::::::::::::::.:        ::.        :.:::
       -------GTGGTCGGCCCCCAGCGACCCCCTGGA----------GCT---------TGTG----------
                570       580       590                  600

        980       990      1000      1010      1020      1030      1040
inputs CCTGTCAGCACAGCCGGGCCCCACAGTGGCCTCAGGAGAGAACGTGACCCTGCTGTGTCAGTCATGGTGG
       ::::          :.::  ::..:.:::.::                    :::.::      :.::
       ---GTCA-------CAGGAACCTCTGTGACC-----------------CCCAGC-----CGGT--------
                      610       620                     630

       1050      1060      1070      1080      1090      1100      1110
inputs CAGTTTGACACTTTCCTTCTGACCAAAGAAGGGGCAGCCCATCCCCCACTGCGTCTGAGATCAATGTACG
                :.::..:.:: :            ::  ::.:::                        .::
       ------------TACCAACAGAAC----------CA--CCTTCC--------------------TCG
                    640                    650

       1120      1130      1140      1150      1160      1170      1180
```

FIGURE 3b

```
inputs GAGCTCATAAGTACCAGGCTGAATTCCCCATGAGTCCTGTGACCTCAGCCCACGCGGGGACCTACAGGTG
       :..            ::.:::::: :           .:...::.:        ::: :.     ::.: .
       GTA------------GCAGAATTCTC---------AGAAGCCAC------CGCTGA-----ACTG--A
       660                    670                 680             690

       1190      1200      1210      1220      1230      1240      1250
inputs CTACGGCTCATACAGCTCCAACCCCCACCTGCTGTCTTTCCCCAGTGAGCCCCTGGAACTCATGGTCTCA
       :  ::  :::::.::   :  :::          . .:::::  : ::.       :::..:::    :::
       C--CGTCTCATTCA---CAAAC--------AAGTCTT--CACAA-------CTGAGACT-----TCT--
            700                  710       720             730

       1260      1270      1280      1290      1300      1310      1320
inputs GGACACTCTGGAGGCTCCAGCCTCCCACCCACAGGGCCGCCCTCCACACCTGGTCTGGGAAGATACCTGG
       .  .:::: ::   .::.:: . ::: :::.   : :   :.:.::.:  ^  :
       --------AGGAGTATC--ACCACCAGTCCAAAGGA--GTCAGACTCTCCAG--CTGG------------
              740         750         760         770

       1330      1340      1350      1360      1370      1380      1390
inputs AGGTTTTGATTGGGGTCTCGGTGGCCTTCGTCCTGCTGCTCTTCCTCCTCCTCTTCCTCCTCCTCCGACG
                                          ::::::          :: ::.:.    :: :..::.: :
       ----------------------------------TCCTGC--------CCGCCAGTA-----CTACACCAAGG
                                         780              790           800

       1400      1410      1420      1430      1440      1450      1460
inputs TCAGCGTCACAGCAAACACAGGACATCTGACCAGAGAAAGACTGATTTCCAGCGTCCTGCAGGGGCTGCG
       ::.:            :.::.:              : :::.:  :: ::   :::::::
       GCAAC-----------CTGGTC-------------CGGATAT---GCCTC-----GGGGCTG--
           810                          820            830

       1470      1480      1490      1500      1510      1520      1530
inputs GAGACAGAGCCCAAGGACAGGGGCCTGCTGAGGAGGTCCAGCCCAGCTGCTGACGTCCAGGAAGAAAACC
       .:: :: :: .:       :::: : ::.: : :.:      ::.:: : :.::       :
       ----TGATCCTAATAA-----TCCTG--GCGGGGTTTCTG-------GCAGA-GGACTGG--------C
           840         850       860             870

       1540      1550      1560      1570      1580      1590      1600
inputs TCTATGCTGCCGTGAAGGACACACAGTCTGAGG-ACAGGGTGGAGCTGGACAGT-CAGAGCCCACACGAT
       .:     .:::::  .::::: .:.:  ::: :: ::::::         ::.::::.:: :::::: ::..:.
       AC-----AGCCG--GAGGAAGCGC---CTGCGGCACAGGG----GCAGGGCTGTGCAGAGGCCGCT----
             880         890       900             910       920

       1610      1620      1630      1640      1650      1660      1670
inputs GAAGACCCCCAGGCAGTGACGTATGCCCCGGTGAAACACTCCAGTCCTAGGAGAGAAATGGCCTCTCCTC
       .::            :::::: :                                   :: :    :
       ----TCC-----------------GCCCCTG---------------------------CCGC----C
            930                                                  940

       1680      1690      1700      1710      1720      1730      1740
inputs CCTCCTCACTGTCTGGGGAATTCCTGGACACAAAGGACAGACAGGTGGAAGAGGACAGGCAGATGGACAC
       :::::  :.:.:.:           :: :.: .::      ::  :.::      ::.:::::  :::::
       CCTCC--CGCAGAC----------CCGGAAATCA------CA--CGGG-------GGTCAGG---ATGGA---
       950                  960             970       980
```

FIGURE 3c

```
        1750        1760        1770        1780        1790        1800        1810
inputs  TGAGGCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCCCAGCTGCACAGCTTGACCCTTAGACGG
        :::         :..:        :::::::                   ::::::            .::
        ---GGC-----CGAC-----------AGGATGTT----------------CACAGC-----------CG-
                                      990                    1000

        1820        1830        1840        1850        1860        1870        1880
inputs  AAGGCAACTGAGCCTCCTCCATCCCAGGAAGGGGAACCTCCAGCTGAGCCCAGCATCTACGCCACTCTGG
                                     :.::... :                      .::.
        -----------------------------CGGGTTATG---------------------TTCA-----------
                                       1010

        1890
inputs  CCATCCAC

        --------
```

FIGURE 3d

```
ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> hT268 a.a.                                     339 aa vs.
> GenPept U91928 - Human clone HL9 monocyte inhib   631 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
23.0% identity;          Global alignment score: -647

               10        20        30        40        .50        60
inputs  MSPSPTALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLEKLSSS----
        :.:. :::.:::: :: :. .:.::.:::.: : :.:... :::..:::. .. :::.: .:.
        MTPALTALLCLGLSLGPRTRVQAGPFPKPTLWAEPGSVISWGSPVTIWCQGSLEAQEYRLDKEGSPEPLD
          10        20        30        40        50        60        70

               70        80        90        100       110  . '_ 120      130
inputs  RYQ-----DQAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDV
        : .     ..: . ::.: :::::: : ... :: :::.:::: :: ..::.::: :.:.:.:::..:
        RJNPLEPKNKARFSIPSMTEHHAGRYRCHYYSSAGWSEPSDPLELVMTGFYNKPTLSALPSPVVASGGNM
          80        90        100       110       120       130       140

inputs  TLQCQT------------------------------------------------RY---------------
        ::.:. .
        TLRCGSQKGYHHFVLMKEGEHQLPRTLDSQQLHSGGFQALFPVGPVNPSHRWRFTCYYYYMNTPQVWSHP
          150       160       170       180       190       200       210

                                                        140       150
inputs  ----------------------------------------GFDQFALYKEGDP------------------
                                                :.:.:.:::::.
        SDPLEILPSGVSRKPSLLTLQGPVLAPGQSLTLQCGSDVGYDRFVLYKEGERDFLQRPGQQPQAGLSQAN
          220       230       240       250       260       270       280

                                                                         160
inputs  -----------APYK-------------NP------------------------------ERW--
                    ..:.              .:                              . :
        FTLGPVSPSHGGQYRCYGAHNLSSEWSAPSDPLNILMAGQIYDTVSLSAQPGPTVASGENVTLLCQSWWQ
          290       300       310       320       330       340       350

                                        170       180       190       200
inputs  ------------------------YRASFPIITVTAAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTG
                                :.: ::.  ::.::.:::::. : .: : : ::.:::.:.:
        FDTFLLTKEGAAHPPLRLRSHYGAHKYQAEFPHSPVTSAHAGTYRCYGSYSSNPHLLSFPSEPLELHVSG
          360       370       380       390       400       410       420

            210       220       230             240       250       260
inputs  TSVTPSRLPTEPPSS--VAEFSEATAELTVSFTNKVF--------TTETSRSITTSPKESD--SPAGPA-
        : .: :: :::. .. . :. ..:.:. .:          :. :..... .: ::!.:
        HSGGSSLPPTGPPSTPGLGRYLEVLIGVSVAFVLLLFLLLFLLLRRQRHSKHRTSDQRKTDFQRPAGAAE
          430       440       450       460       470       480       490

            270       280       290
inputs  RQYYTKGNLVRICLGAVIL-----IILAGFLAEDW--------------------HSRRKR--------
        .  .:: :  .: .        .. .::.              :: .:
```

<div align="center">

FIGURE 4a

</div>

```
            TEPKDRGLLRRSSPAADVQEENLYAAVKDTQSEDRVELDSQSPHDEDPQAVTYAPVKHSSPRREHASPPS
                  500          510          520          530          540 ·    550          560

                  300                                      310          320              330
        inputs ------LRHRGRAVQ--RPL---------------PPLPPLPQTRK------SHGGQDGGRQDVHSRGLC
                 :   ..: :.   :..                 ..: .:   ::        :. :.   .  ... .
               SLSGEFLDTKDRQVEEDRQHDTEAAASEASQDVTYAQLHSLTLRRKATEPPPSQEGEPPAEPSIYATLAI
                  570          580          590          600          610          620          630

        inputs S

               H
```

FIGURE 4b

```
Alignments of top-scoring domains:
ig: domain 1 of 2, from 41 to 90: score 4.1, E = 6.1
                  *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                    .+ vtL+C+         + v  y +  k  ++        r++ +
       hT268    41   EKPVTLRCQGP------PGVDLY-RLEKlSSS--------RYQDQ-- 70

                  anlsegrfsissltLtissvekeDsGtYtCvv<-.
                    ++L i   +++  +G Y+C
       hT268    71  -----------AVLFIPAMKRSLAGRYRCSY    90
```

FIGURE 5A

```
ig: domain 2 of 2, from 127 to 182: score 19.1, E = 0.1
                   *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                      G++vtL+C+++    +   ++  y k+g++ +      y+++
           hT268  127    GGDVTLQCQTR---YGFDQFALY-KEGDpAP-----YKNPERWYR-- 162

                   anlsegrfsissltLtissvekeDsGtYtCvv<-*
                      ++++i++v++   sGtY+C
           hT268  163 -----------ASFPIITVTAAHSGTYRCYS    182
```

FIGURE 5B

```
                                                                            M   S   P   A      <
GAGTCGACCCACGCGTCCGCTTCCCTGCTTGGCCACATAGCTCAGGACTGGGTTGCAGAACC ATG TCT CCA GCC     74
  S   P   T   F   F   C   I   G   L   C   V   L   Q   V   I   Q   T   Q   S   G      2<
TCA CCC ACT TTC TTC TGT ATT GGG CTG TGT GTA CTG CAA GTG ATC CAA ACA CAG AGT GGC    13<
  P   L   P   K   P   S   L   Q   A   Q   P   S   S   L   V   P   L   G   Q   S      <<
CCA CTC CCC AAG CCT TCC CTC CAG GCT CAG CCC AGT TCC CTG GTA CCC CTG GGT CAG TCA    19<
  V   I   L   R   C   Q   G   P   P   D   V   D   L   Y   R   L   E   K   L   K      6<
GTT ATT CTG AGG TGC CAG GGA CCT CCA GAT GTG GAT TTA TAT CGC CTG GAG AAA CTG AAA    25<
  P   E   K   Y   E   D   Q   D   F   L   F   I   P   T   H   E   R   S   N   A      8<
CCG GAG AAG TAT GAA GAT CAA GAC TTT CTC TTC ATT CCA ACC ATG GAA AGA AGT AAT GCT    31<
  G   R   Y   R   C   S   Y   Q   N   G   S   H   W   S   L   P   S   D   Q   L     10<
GGA CGG TAT CGA TGC TCT TAT CAG AAT GGG AGT CAC TGG TCT CTC CCA AGT GAC CAG CTT    37<
  E   L   I   A   T   G   V   Y   A   K   P   S   L   S   A   H   P   S   S   A     12<
GAG CTA ATT GCT ACA GGT GTG TAT GCT AAA CCC TCA CTC TCA GCT CAT CCC AGC TCA GCA    43<
  V   P   Q   G   R   D   V   T   L   K   C   Q   S   P   Y   S   F   D   E   F     14<
GTC CCT CAA GGC AGG GAT GTG ACT CTG AAG TGC CAG AGC CCA TAC AGT TTT GAT GAA TTC    49<
  V   L   Y   K   E   G   D   T   G   P   Y   K   R   P   E   K   W   Y   R   A     16<
GTT CTA TAC AAA GAA GGG GAT ACT GGG CCT TAT AAG AGA CCT GAG AAA TGG TAC CGG GCC    55<
  N   F   P   I   I   T   V   T   A   A   H   S   G   T   Y   R   C   Y   S   F     18<
AAT TTC CCC ATC ATC ACA GTG ACT GCT GCT CAC AGT GGG ACG TAC CGG TGT TAC AGC TTC    61<
  S   S   S   S   P   Y   L   W   S   A   P   S   D   P   L   V   L   V   V   T     20<
TCC AGC TCA TCT CCA TAC CTG TGG TCA GCC CCG AGT GAC CCT CTA GTG CTT GTG GTT ACT    67<
  G   L   S   A   T   P   S   Q   V   P   T   E   E   S   F   P   V   T   E   S     22<
GGA CTC TCT GCC ACT CCC AGC CAG GTA CCC ACG GAA GAA TCA TTT CCT GTG ACA GAA TCC    73<
  S   R   R   P   S   I   L   P   T   N   K   I   S   T   T   E   K   P   H   N     24<
TCC AGG AGA CCT TCC ATC TTA CCC ACA AAC AAA ATA TCT ACA ACT GAA AAG CCT ATG AAT    79<
  I   T   A   S   P   E   G   L   S   P   P   I   G   F   A   H   Q   H   Y   A     26<
ATC ACT GCC TCT CCA GAG GGG CTG AGC CCT CCA ATT GGT TTT GCT CAT CAG CAC TAT GCC    85<
  K   G   N   L   V   R   I   C   L   G   A   T   I   I   I   I   L   L   G   L     28<
AAG GGG AAT CTG GTC CGG ATA TGC CTT GGT GCC ACG ATT ATA ATA ATT TTG TTG GGG CTT    91<
  L   A   E   D   W   H   S   R   K   K   C   L   Q   H   R   H   R   A   L   Q     30<
CTA GCA GAG GAT TGG CAC AGT CGG AAG AAA TGC CTG CAA CAC AGG ATG AGA GCT TTG CAA    97<
  R   P   L   P   P   L   P   L   A   *                                            31<
AGG CCA CTA CCA CCC CTC CCA CTG GCC TAG                                           100<

AAATAACTTGGCTTTCAGCAGAGGGATTGACCAGACATCCATGCACAACCATGGACATCACCACTAGAGCCACAGACAT  1083

GGACATACTCAAGAGTGGGGAGGTTATATAAAAAAAATGAGTGTGGAGAATAAATGCAGAGCCAACAAGGTGAAAAAAAA  1162

A
                                                                                  1163
```

FIGURE 6

Cut
Kgle
out

```
  1      41      81      121    161    201    241    281
```
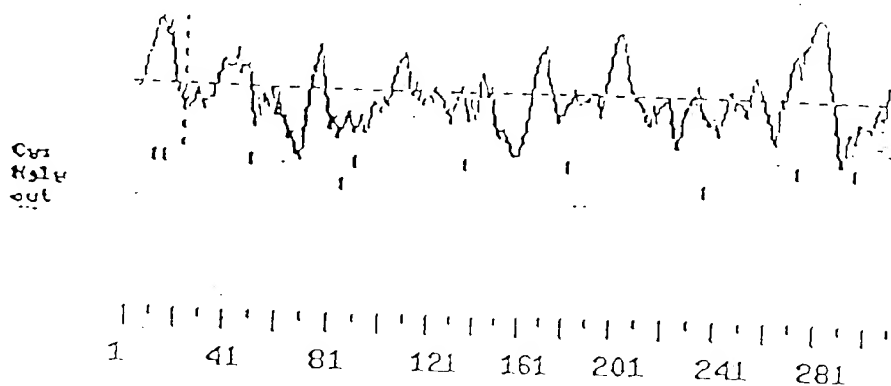
MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRL
EKLKPEKYEDQDFLFIPTMERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAH
PSSAVPQGRDVTLKCQSPYSFDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAAHSGTYR
CYSFSSSSPYLWSAPSDPLVLVVTGLSATPSQVPTEESFPVTESSRRPSILPTNKISTTE
KPMNITASPEGLSPPIGFAHQHYAKGNLVRICLGATIIIILLGLLAEDWHSRKKCLQHRM
RALQRPLPPLPLA

FIGURE 7

```
ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> U91928 ORF
                                           1893 aa vs.
> mT268 ORF
                                           939 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
34.3% identity;          Global alignment score: -836

            10        20        30        40        50        60        70
inputs ATGACGCCCGCCCTCACAGCCCTGCTCTGCCTTGGGCTGAGTCTGGGCCCCAGGACCCGCGTGCAGGCAG
       :::.: :: ::: :::: ::    .:: :::   :::.. :
       ATGTCTCCAGCC-TCAC--CC----ACTTTCTT---CTGTAT--------------------------
            10        20        30

            80        90        100       110       120       130       140
inputs GGCCCTTCCCCAAACCCACCCTCTGGGCTGAGCCAGGCTCTGTGATCAGCTGGGGGAGCCCCGTGACCAT
                        :::::::                :::::..:.::
       -----------------------------TGGGCTG---------TGTGTACTGC-------------
                                                   40

            150       160       170       180       190       200       210
inputs CTGGTGTCAGGGGAGCCTGGAGGCCCAGGAGTACCGACTGGATAAAGAGGGAAGCCCAGAGCCCTTGGAC
                                   :.:.:..::                 ::..: :::::  :::
       -----------------------AAGTGATCC----------------AAACACAGAG----TGG--
                                        50                  60        70

            220       230       240       250       260       270       280
inputs AGAAATAACCCACTGGAACCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCGG
              ::::::    :::    ::::       ::.:::: :::: :
       --------CCCACT----CCC-----CAAG----------CCTTCCC-TCCAGG-------------
              80                                 90

            290       300       310       320       330       340       350
inputs GGAGATACCGCTGCCACTATTACAGCTCTGCAGGCTGGTCAGAGCCCAGCGACCCCCTGGAGCTGGTGAT
            : :.:::                              :::. :::.: :. ::::::::. :.:
       --------CTCAGCC----------------------CAGTTCCCTG-GTACCCCTGGGTCAG-----
            100                                  110       120

            360       370       380       390       400       410       420
inputs GACAGGATTCTACAACAAACCCACCCTCTCAGCCCTGCCCAGCCCTGTGGTGGCCTCAGGGGGGAATATG
       .::: :: :.:                              ::.::::: :  :::::.
       -TCAG--TTATTC-----------------------------TGAGGTG-C--CAGGGA--------
       130                                      140       150

            430       440       450       460       470       480
inputs ACCCTCC-GATGTGGCTCACAGAAGGGATATCACCATTTTGTTCTGATGAAGGAAGGAGAACACCAGCTC
       ::::: :::::::              :  :::::.::.  . ...:::::..
       --CCTCCAGATGTGG--------ATTTATATCGCCTGGAGAAACTGAAA--------------------
           160                   170       180       190

       490       500       510       520       530       540       550
inputs CCCCGGACCCTGGACTCACAGCAGCTCCACAGTGGGGGGTTCCAGGCCCTGTTCCCTGTGGGCCCCGTGA
       :::::        ::                ::::. :..:.:: ::.:      ::: ::      :.:
```

FIGURE 8a

```
       --CCGGA-----GA----------------AGTATGAAGATCAAGAC---TTTCTCTT-------CATT-
                                   200        210         220

        560       570       580       590       600       610       620
inputs ACCCCAGCCACAGGTGGAGGTTCACATGCTATTACTATTATATGAACACCCCCCAGGTGTGGTCCCACCC
        :::.::: .:...::.:.   :::::           :.::           :::.:
       ---CCAACCATGGAAAGAAGTA---ATGCT-------------GGAC-------GGTAT---------
        230       240       250                                  260

        630       640       650       660       670       680       690
inputs CAGTGACCCCCTGGAGATTCTGCCCTCAGGCGTGTCTAGGAAGCCCTCCCTCCTGACCCTGCAGGGCCCT
        :..::  : ::.          ::::.      ..::.:: :              .:.:: : ::
       CGATG---CTCTTA-----------TCAGA------ATGGGAGTC---------------ACTGGTCTCT
            270                    280                                290

        700       710       720       730       740       750       760
inputs GTCCTGGCCCCTGGGCAGAGCCTGACCCTCCAGTGTGGCTCTGATGTCGGCTACGACAGATTTGTTCTGT
        :::..:       ::::: : .:.:    ::..::   :::::
       -------CCCAAG---------TGACCAGCTTGAG-----CTAATT---GCTAC---------------
            300              310           320

        770       780       790       800       810       820       830
inputs ATAAGGAGGGGGAACGTGACTTCCTCCAGCGCCCTGGCCAGCAGCCCCAGGCTGGGCTCTCCCAGGCCAA
        :::.: : ...: ..:: ::::                           .:::::
       ---AGGTGTGTATGCTAAAC--CCTC-----------------------ACTCTC---------
          330       340                                 350

        840       850       860       870       880       890       900
inputs CTTCACCCTGGGCCCTGTGAGCCCCTCCCACGGGGGCCAGTACAGGTGCTATGGTGCACACAACCTCTCC
                   ::: : :::::                       :::
       -----------------AGCTCATCCCA-----------------GCT--------------------
                       360

        910       920       930       940       950       960       970
inputs TCCGAGTGGTCGGCCCCCAGCGACCCCCTGAACATCCTGATGGCAGGACAGATCTATGACACCGTCTCCC
             :::::.. :::      ::   :.::::::   :::  .::::.: :.
       ---------------CAGCAGTCCC-------TC---AAGGCAGG---GAT--GTGACTCTGA-----
                    370            380         390          400

        980       990      1000      1010      1020      1030      1040
inputs TGTCAGCACAGCCGGGCCCCACAGTGGCCTCAGGAGAGAACGTGACCCTGCTGTGTCAGTCATGGTGGCA
        .::      :::.:. :::: :                       :::: .::.::.
       AGT------GCCAGAGCCCATA----------------------------CAGTTTTGATGA--
               410                                       420

       1050      1060      1070      1080      1090      1100      1110
inputs GTTTGACACTTTCCTTCTGACCAAAGAAGGGGCAGCCCATCCCCCACTGCGTCTGAGATCAATGTACGGA
        .::: :::::.. ::::::::::::    ::     :::: : :: : : :...:. : ::
       ---------ATTCGTTCTATACAAAGAAGGGG------AT-----ACTGGGCCTTATA--AGAGACCTGA
               430       440       450              460       470

       1120      1130      1140      1150      1160      1170      1180
```

FIGURE 8b

```
inputs GCTCATAAGTACCAGGCTGAATTCCCCATGAGTCCTGTGACCTCAGCCCACGCGGGGACCTACAGGTGCT
       : :...::::.::: .:.:::::::::: :   :.:::: :.::::::. ::::: ::: :::: :
       G--AAATGGTACCGGGCCAATTTCCCCATCATCACAGTGACTGCTGCTCACAGTGGGACGTACCGGTGTT
         480        490        500        510        520        530        540

   1190       1200       1210       1220       1230       1240       1250
inputs ACGGCTCATACAGCTCCAACCCCCACCTGCTGTCTTTCCCCAGTGAGCCCCTGGAACTCATGGTCTCAGG
       ::.::: : :::::: . :: ::::: :::. ::: :::::: :: ::.:..:: .:::: .:.::
       ACAGCTTCTCCAGCTCATCTCCATACCTGTGGTCAGCCCCGAGTGACCCTCTAGTGCTTGTGGTTACTGG
         550        560        570        580        590        600        610

   1260       1270       1280       1290       1300       1310       1320
inputs ACACTCTGGAGGCTCCAGCCTCCCACCCACAGGGCCGCCCTCCACACCTGGTCTGGGAAGATACCTGGAG
       ::.:::::   ::: :::::: :: :::   .:::.: ::. .:... ..:.::::
       ACTCTCTG------CCA--CTCCCAGCC--AGGT--ACCCAC-------GGA-AGAATCATTTCCTG---
         620            630          640              650        660

   1330       1340       1350       1360       1370       1380       1390
inputs GTTTTGATTGGGGTCTCGGTGGCCTTCGTCCTGCTGCTCTTCCTCCTCCTCTTCCTCCTCCTCCGACGTC
       :::        :.:.. :::   ::.: .: :::::.    ::::  :   ::: .::..
       ----TGA---------CAGAATCCT----CCAGGAGACCTTCCA-----TCTTAC----CCACAAACAAA
                       670          680             690             700

   1400       1410       1420       1430       1440       1450       1460
inputs AGCGTCACAGCAAACACAGGACATCTGACCAGAGAAAGACTGATTTCCAGCGTCCTGCAGGGGCTGCGGA
       :  : .:..::: :..:.: ...:...::::..: : ::. : ::::.: :::::::::
       A---TATCTACAA---CTGAA----AAGCCTATGAATATC--ACTGCCT-C-TCCAG-AGGGGCTG----
         710        720          730          740              750

   1470       1480       1490       1500       1510       1520       1530
inputs GACAGAGCCCAAGGACAGGGGCCTGCTGAGGAGGTCCAGCCCAGCTGCTGACGTCCAGGAAGAAAACCTC
       :::::.        ::    :. .::: .:: :: :.::.                          :
       -----AGCCCT----------CC-----AATTGGTTTTGCTCATCAGCA--------------------C
         760                    770        780

   1540       1550       1560       1570       1580       1590       1600
inputs TATGCTGCCGTGAAGGACACACAGTCTGAGGACAGGGTGGAGCTGGACAGTCAGAGCCCACACGATGAAG
       :::::                        ::.:: :.: :::::.:                  ::.. ::
       TATGC---------------------------CAAGGGGAATCTGGTC-------------CGGATATG
         790                               800                    810

   1610       1620       1630       1640       1650       1660       1670
inputs ACCCCCAGGCAGTGACGTATGCCCCGGTGAAACACTCCAGTCCTAGGAGAGAAATGGCCTCTCCTCCCTC
        :: .::           :::: ::.:             :: .: :.....::
       ---CCTTGG----------TGCCACGAT---------------TATAATAATTTTGT-------------
         820              830                      840

   1680       1690       1700       1710       1720       1730       1740
inputs CTCACTGTCTGGGGAATTCCTGGACACAAAGGACAGACAGGTGGAAGAGGACAGGCAGATGGACACTGAG
       :::::.: ::.: ::.:::: .:.:                   :::: :..::.:.:         :
       ---------TGGGGCTT--CTAG---CAGAGGATTGGC-----------ACAGTCGGAAGAA-----AT
         850          860                               870        880
```

FIGURE 8c

```
        1750        1760        1770        1780        1790        1800        1810
inputs GCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCCCAGCTGCACAGCTTGACCCTTAGACGGAAGG
        ::   :::::.:.            :::::::.::                        ::::  .:           .::::
        GC--CTGCAACA---------CAGGATGAGA-------------------GCTTTGC---------AAAGG
            890                     900                                  910

        1820        1830        1840        1850        1860        1870        1880
inputs CAACTGAGCCTCCTCCATCCCAGGAAGGGGAACCTCCAGCTGAGCCCAGCATCTACGCCACTCTGGCCAT
        :  :::.      ::.:::              :::::                       :.::::::::
        CCACTA-----CCACC----------------CCTCC-------------------------CACTGGCC--
            920                        930

        1890
inputs CCAC

        ----
```

FIGURE 8d

```
ALIGN calculates a global alignment of two sequences
  version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> mT268 a.a.                                        313 aa vs.
> GenPept U91928 - Human clone HL9 monocyte inhib   631 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
20.3% identity;          Global alignment score: -802

            10        20        30        40        50        60
inputs MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRLEKL-KPERYE
       :..::    ...:.::  . .  ...:.::.:::.:  :.:.::... :  .:..::::. ... ::: ::
       MTPALTALLCLGLSLGPRTRVQAGPFPKPTLWAEPGSVISWGSPVTIWCQGSLEAQEYRLDKEGSPEPLD
            10        20        30        40        50        60        70

        70             80        90        100       110      120       130
inputs DQDFL-------F-IPTMERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAHPSSAVPQGRDV
       .. :      : ::.:  .::::::: :  ... :: :.::.::: ::..:. : ..
       RNNPLEPKNKARFSIPSMTEHHAGRYRCHYYSSAGHSEPSDPLELVHTGFYNKPTLSALPSPVVASGGNY
             80        90        100       110       120      130       140

inputs TLRC--QSPY--------------------------------------------------------------
       ::.:  :  :
       TLRCGSQKGYHHFVLMKEGEHQLPRTLDSQQLHSGGFQALFPVGPVNPSHRWRFTCYYYYMITPQVWSHP
              150       160       170       180       190       200       210

                                            140       150
inputs -----------------------------------------SFDEFVLYKEGD-----------------
                                              ..: ::::::::.
       SDPLEILPSGVSRKPSLLTLQGPVLAPGQSLTLQCGSDVGYDRFVLYKEGERDFLQRPGQQPQAGLSQAN
              220       230       240       250       260       270       280

                                                                      160
inputs ----------TGPYK-----------------------------------RP-------------EKW--
                 :.:.                                    .:              . :
       FTLGPVSPSHGGQYRCYGAHNLSSEWSAPSDPLNILMAGQIYDTVSLSAQPGPTVASGENVTLLCQSWHQ
              290       300       310       320       330       340       350

                                    170       180       190       200
inputs ----------------------------------YRANFPIITVTAAHSGTYRCYSFSSSSPYLWSAPSDPLVLVVTG
                                          :.:.::.  ::.::.:::::.  ::..:  :  :  ::.:: :.:.:
       FDTFLLTKEGAAHPPLRLRSMYGAHKYQAEFPHSPVTSAHAGTYRCYGSYSSNPHLLSFPSEPLELMVSG
              360       370       380       390       400       410       420

        210                       220
inputs LSATPSQVPTEES-----------------FPV---------------------------------------
       :.. .: ::  .                  : .
       HSGGSSLPPTGPPSTPGLGRYLEVLIGVSVAFVLLLFLLLFLLLRRQRHSKHRTSDQRKTDFQRPAGAAE
              430       440       450       460       470       480       490

                  .           230       240       250       260       270
inputs TESS-----RRPS---------ILPTNKISTTEKPHNI-TASPEGLSP-PIGFAH--QHYAKGNLVR--I
       ::.       ::.:          . ..: .   .:   ... . ::  . .: .. .:  .  .. ...
```

FIGURE 9a

```
      TEPKDRGLLRRSSPAADVQEENLYAAVKDTQSEDRVELDSQSPHDEDPQAVTYAPVRHSSPRREMASPPS
           500        510        520        530        540        550       560


           280        290                         300                   310
inputs CLGATIIIILLGLLAEDWH----------------SRKKCLQHRHRALQRPL-----PP--------LPL
       :.. .. .     ..::..                  ..   :   : .: . :        ::       :..
       SLSGEFLDTKDRQVEEDRQMDTEAAASEASQDVTYAQLHSLTLRRKATEPPPSQEGEPPAEPSIYATLAI
           570        580        590        600        610        620       630

inputs A

       H
```

FIGURE 9b

Alignments of top-scoring domains:
ig: domain 1 of 2, from 42 to 91: score 10.2, E = 1.4
```
              *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
              G+sv L+C+              ++v  y +  k ++          +++e +
mT268    42   GQSVILRCQGP------PDVDLY-RLERlKP--------EKYEDQ-- 71

         anlsegrfsissltLtissvekeDsGtYtCvv<-*
              L i +  e++++G  Y+C
mT268    72   -----------DFLFIPTHERSNAGRYRCSY      91
```

FIGURE 10A

```
ig: domain 2 of 2, from 128 to 183: score 9.6, E = 1.6
                  *->GesvtLtCsvsgfgppgvsvthyfkngk.lgpsllgysysrlesgek
          mT268    128   G +vtL C++           ++  y k+g++ +        y+r+e   +
                         GRDVTLKCQSP---YSFDEFVLY-KDGDtGP-------YKRPEKW-Y 162
                                                        _____

                  anlsegrfsissltLtissvekeDsGtYtCvv<-*
          mT268    163  +   .            ++i++v++  sGtY+C
                        RA-----------NFPIITVTAAHSGTYRCYS      183
```

FIGURE 10B

ALIGN calculates a global alignment of two sequences
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> hT268 a.a.   339 aa vs.
> mT268 a.a.   313 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
64.4% identity;   Global alignment score: 1011

```
                10         20         30         40         50         60
inputs  HSPSPTALFCLGLCLGRV-PAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLEKLSSSRYQD
        :::..  ..::.:::.  .:  ..:::::::::::::  ::::::: ..:.:::::::.:::::::::  .
        HSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRLEKLKPEKYED
                10         20         30         40         50         60         70


            70         80         90        100        110        120        130
inputs  QAVLFIPAYKPSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYG
        :.  :::::.:  ::  ::::::::::  :::::::::::.::::.  .:::::::.:...:. :  ::::.::.  :.
        QDFLFIPTHERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAHPSSAVPQGRDVTLKCQSPYS
            80         90        100        110        120        130        140


           140        150        160        170        180        190        200
inputs  FDQFALYKEGDPAPYKNPERWYRASFPIITVTAAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTGTSVTP
        :::..:::::.  .::  :::::::::::::::::::::::::: .::::::::::::: :::::  :.:::
        FDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAAHSGTYRCYSFSSSSPYLWSAPSDPLVLVVTGLSATP
           150        160        170        180        190        200        210


           210        220        230        240        250        260        270
inputs  SRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRSITTSPKESDSPAGPARQYYTKGNLVRICLGAVI
        :..::: . .:.: :      . :   :::. ::: . ..::.:: ..: :.: :.:::::::::.:
        SQVPTEESFPVTESSRRPSILP---TNKISTTEKPHNITASPEGLSPPIGFAHQHYAKGNLVRICLGATI
           220        230        240        250        260        270


           280        290        300        310        320        330
inputs  LIILAGFLAEDWHSRRKRLRHRGRAVQRPLPPLPPLPQTRKSHGGQDGGRQDVHSRGLCS
        .:::  :::::::::.:  :..::  ::.::::::::.:  :.
        IIILLGLLAEDWHSRKKCLQHRHRALQRPLPPLP-LA-------------------------
           280        290        300        310
```

FIGURE 11

kDa

— 200

— 116
— 97

— 67

— 45

— 31
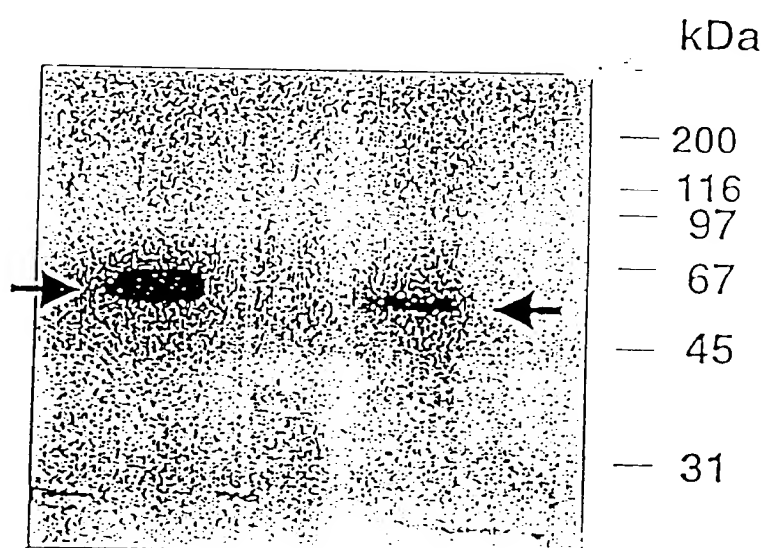
FIGURE 12

FIGURE 13

Sp LN Thy PBL BM FL
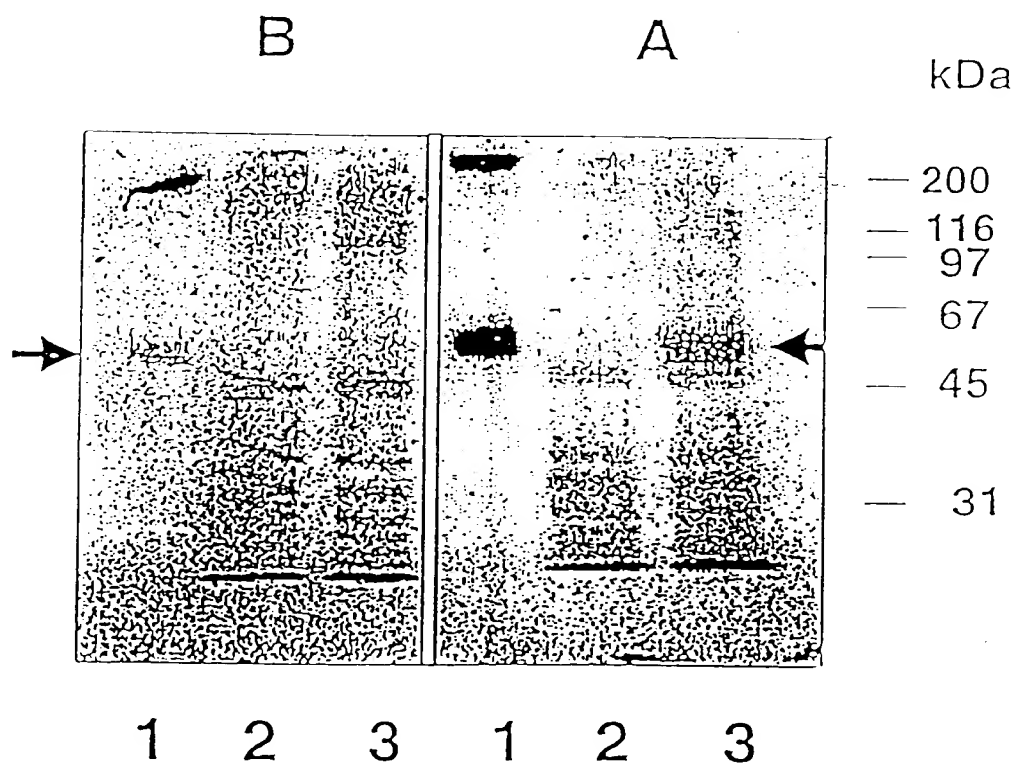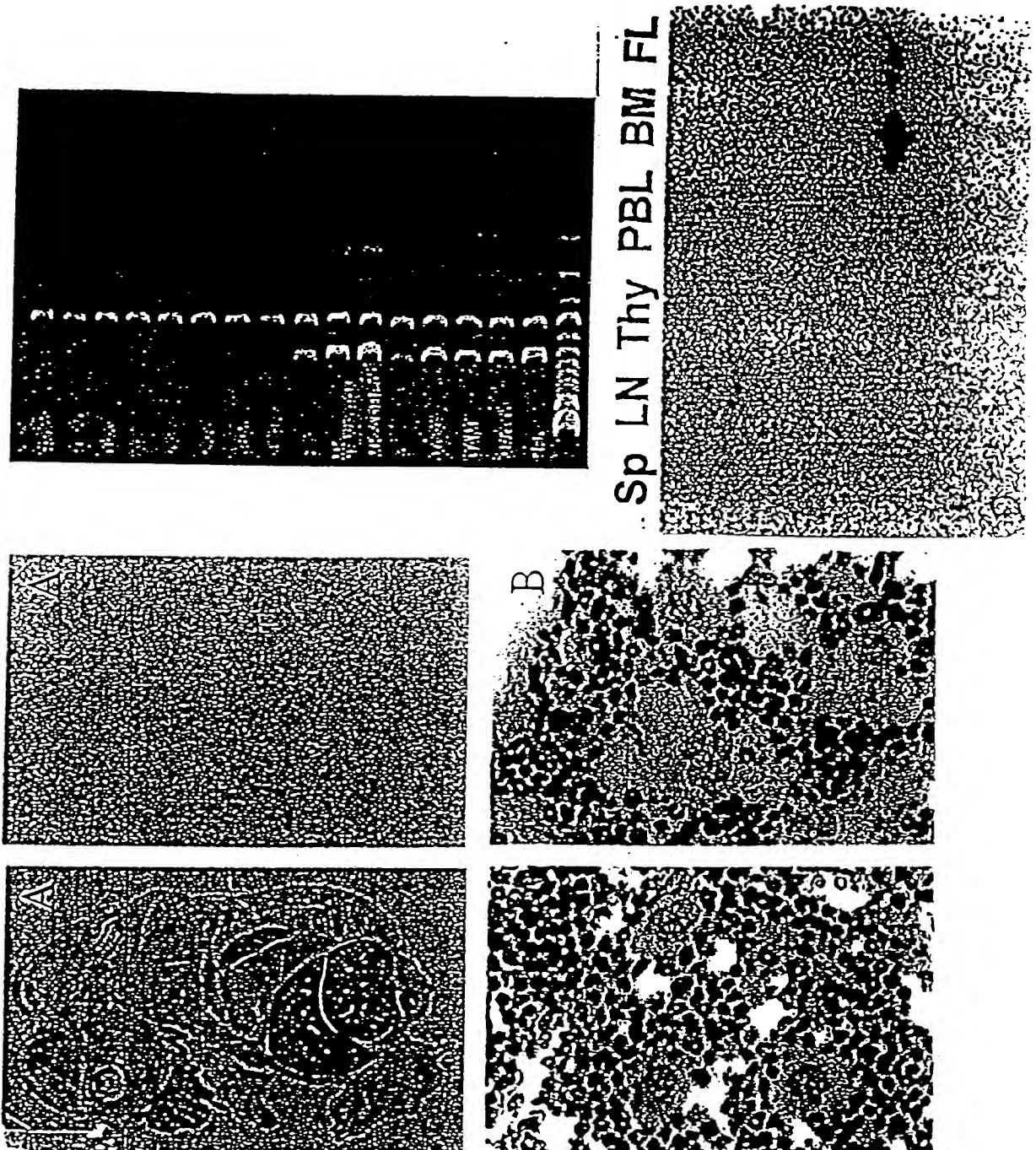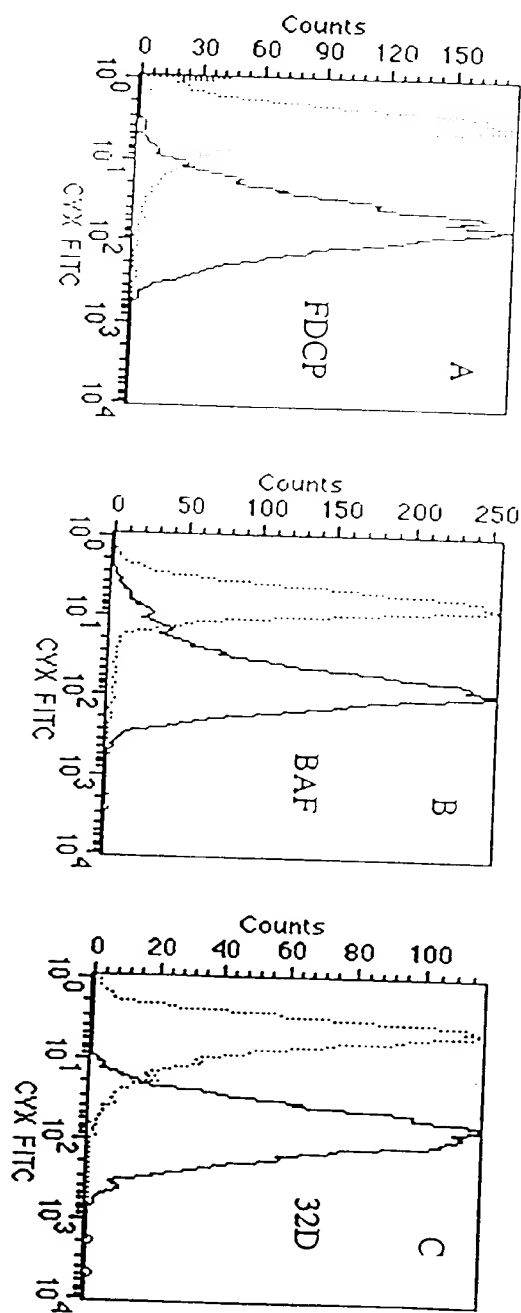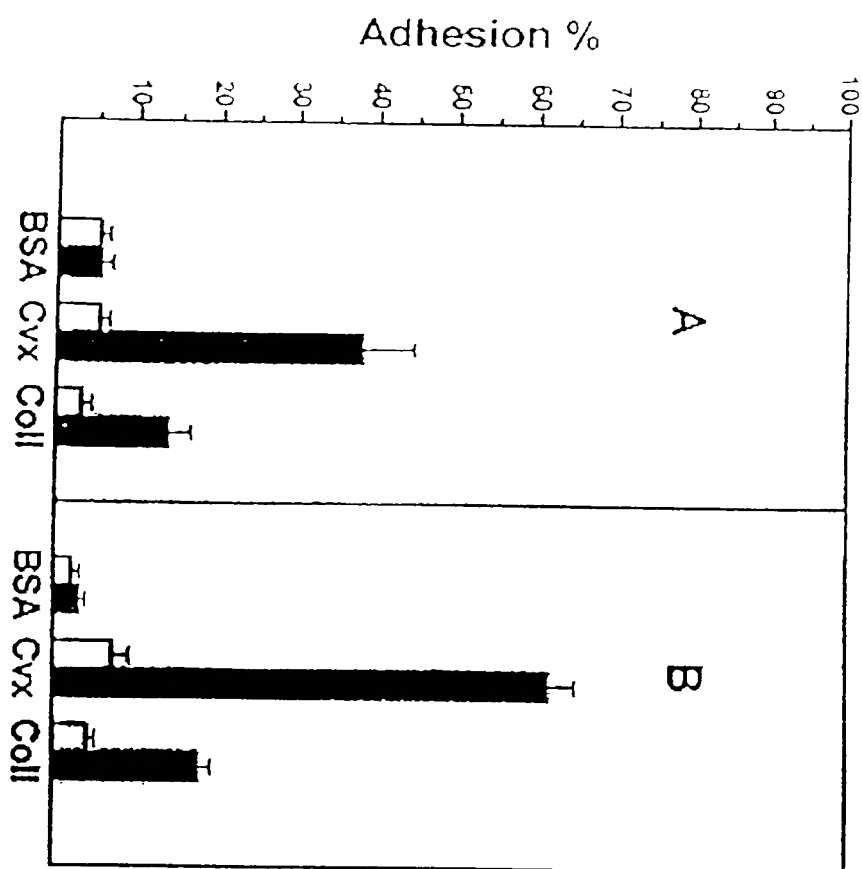
FIGURE 14

FIGURE 15

FIGURE 16
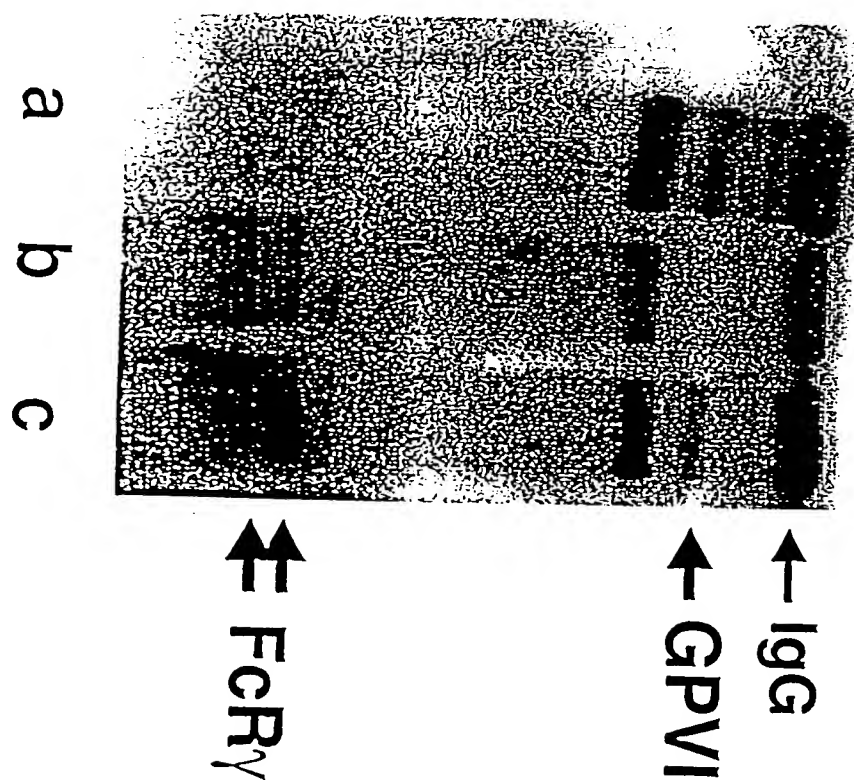
FIGURE 17
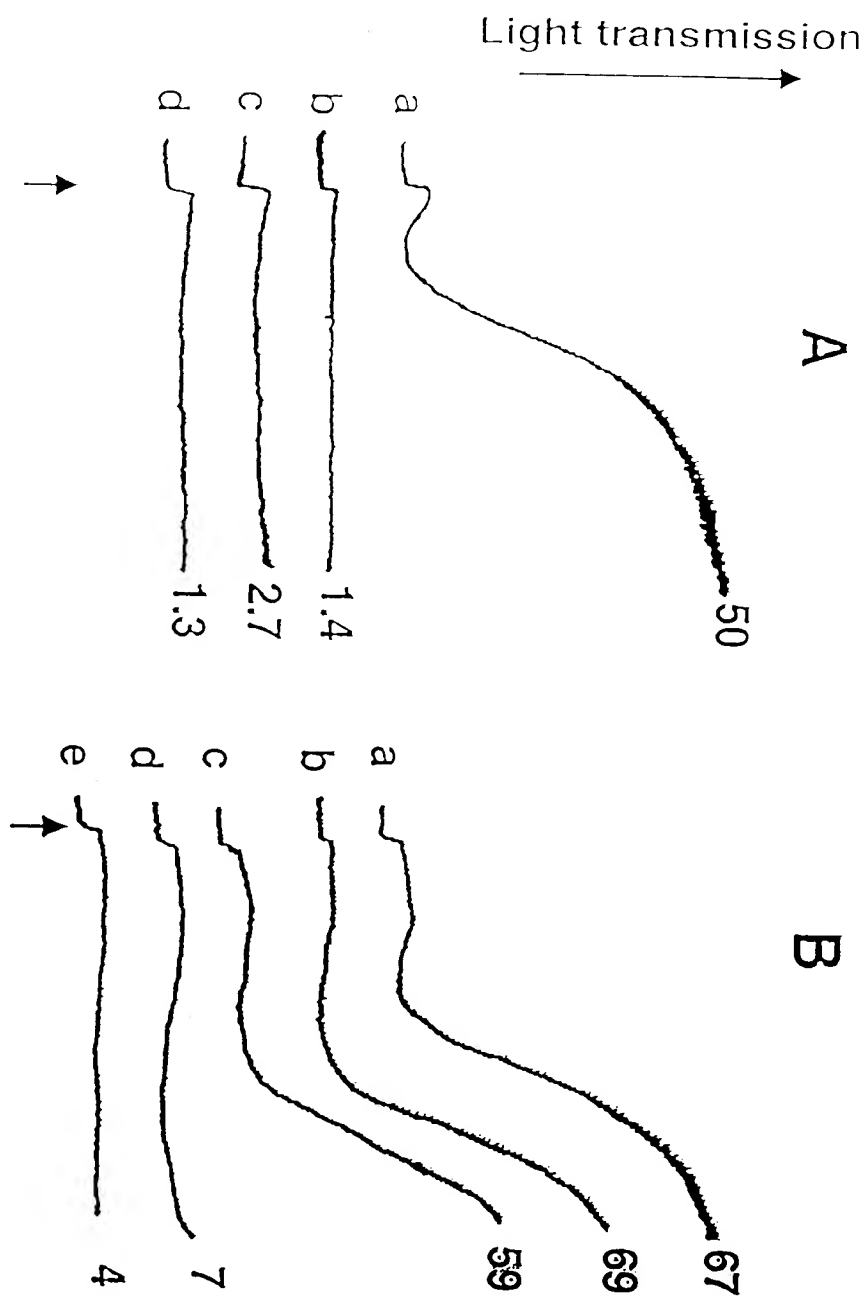
FIGURE 18

FIGURE 19

FIGURE 20

Effet des monoclonaux sur la liaison
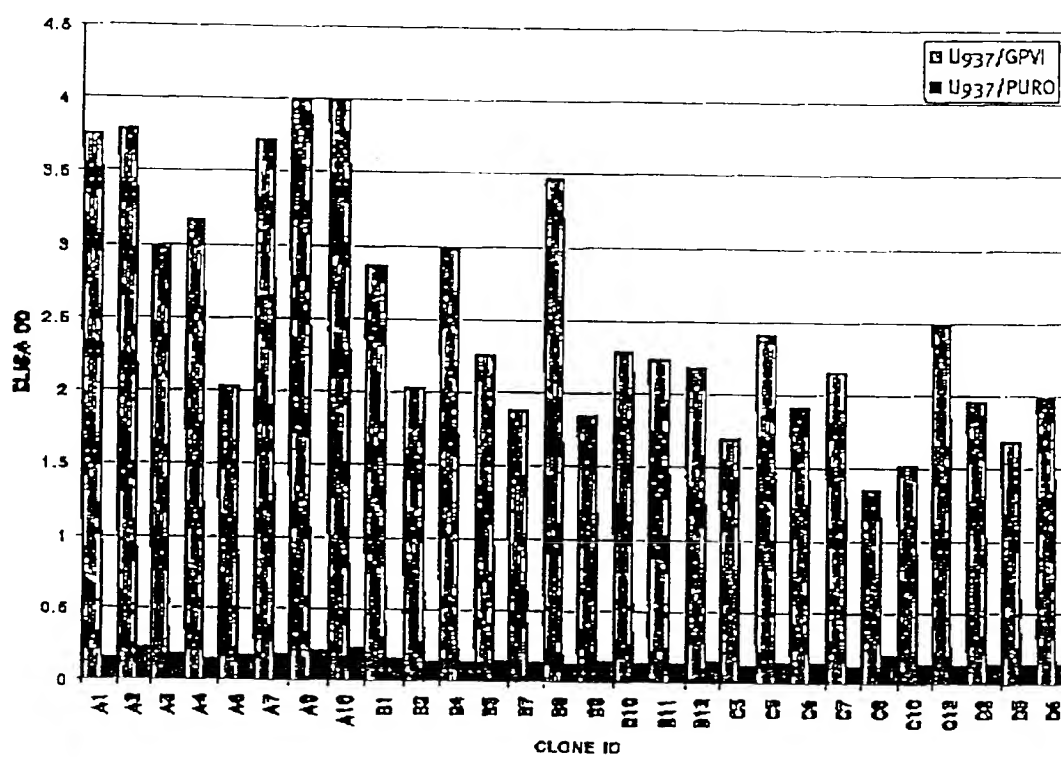GPII-Fc / Convulxine
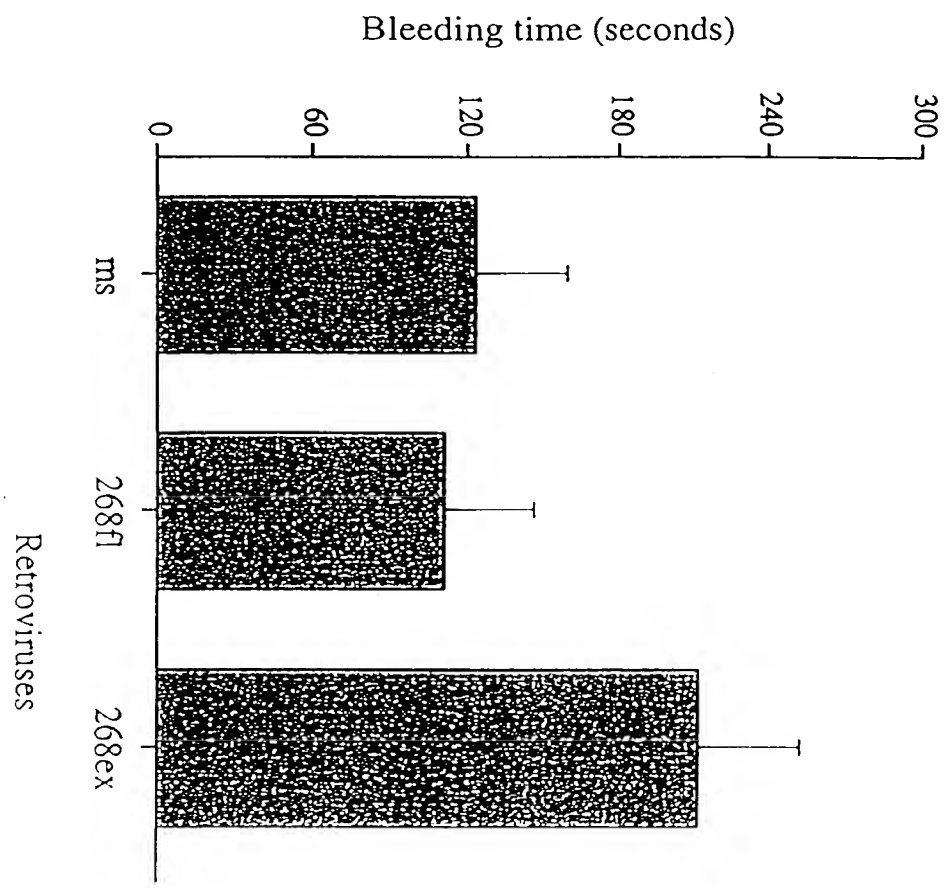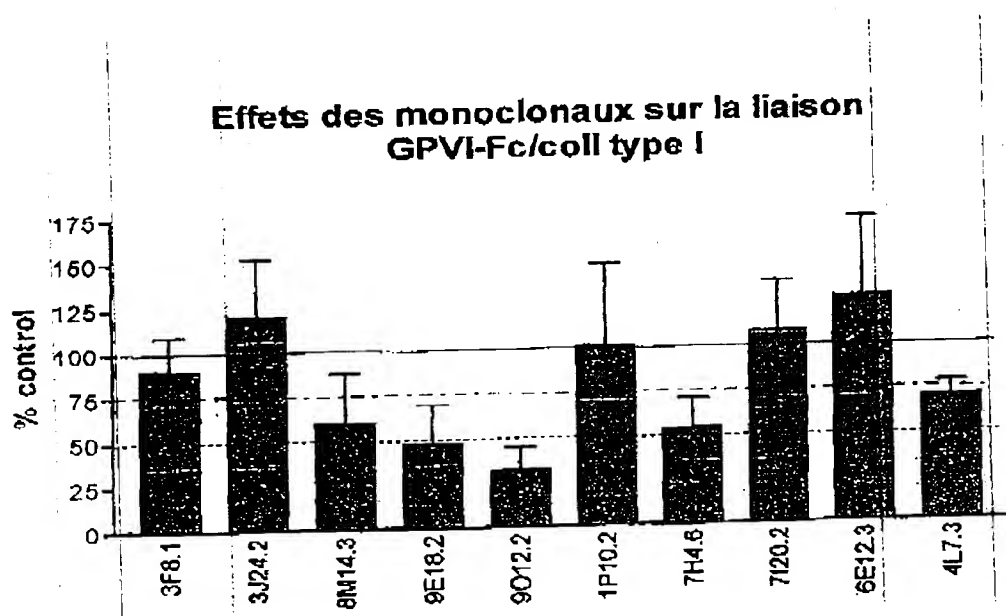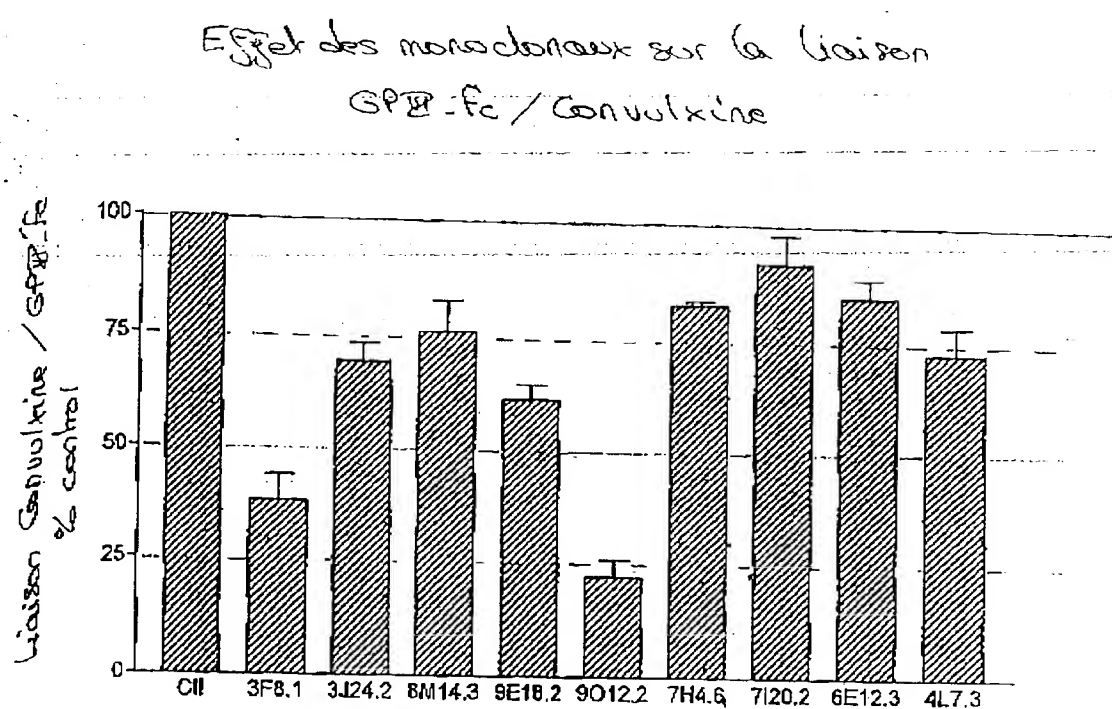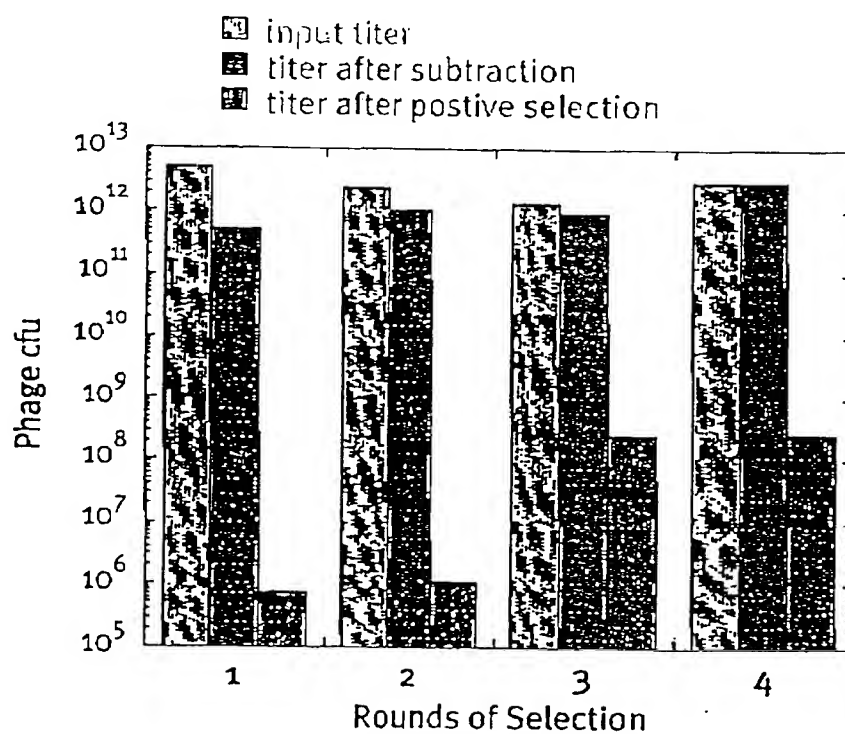
FIGURE 21
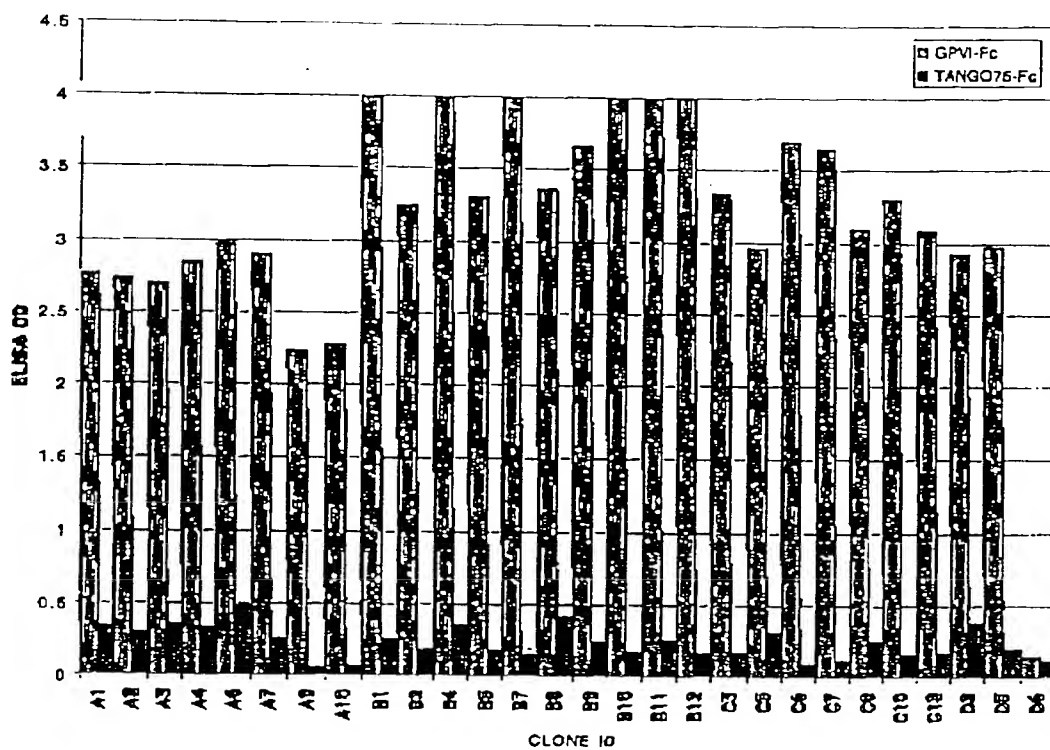
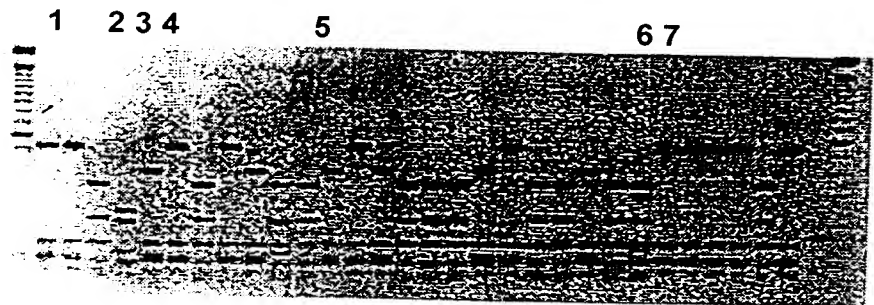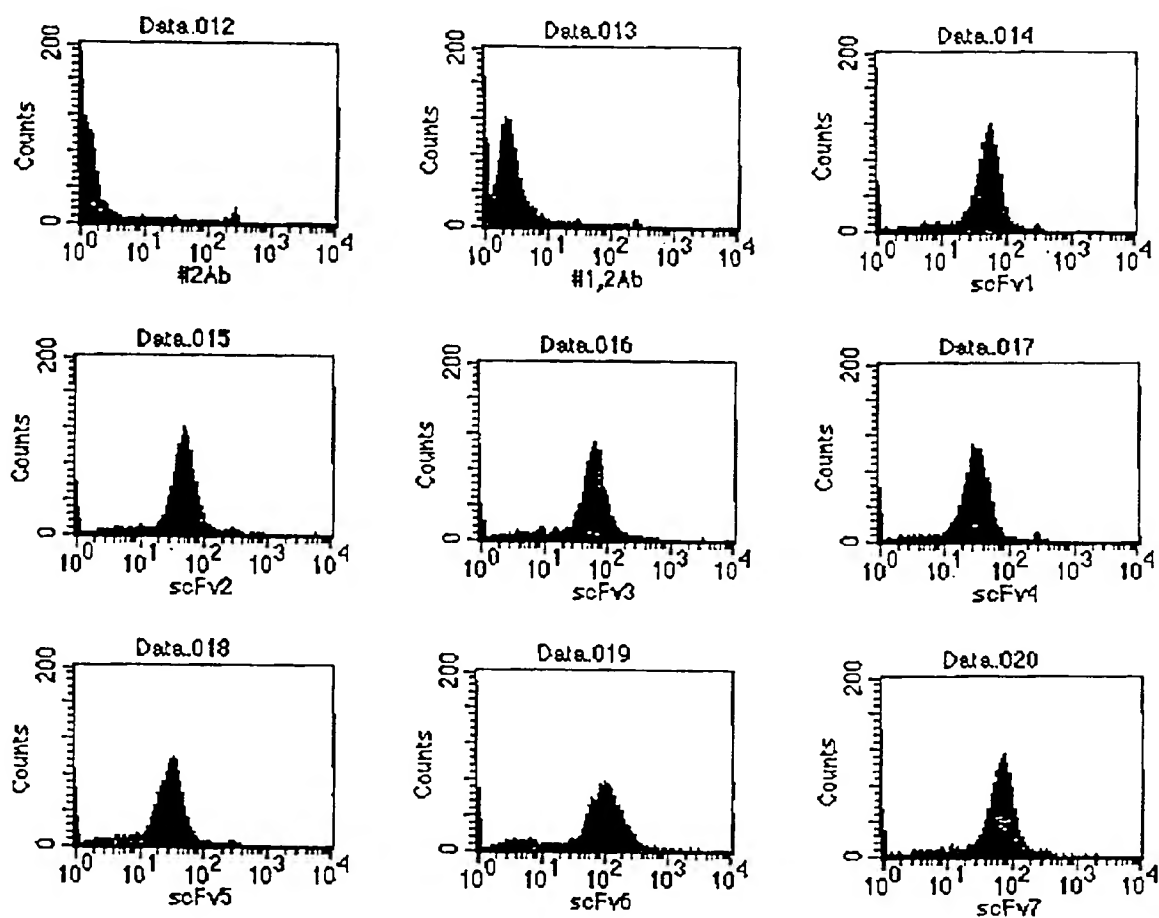**FIGURE 22**

FIGURE 23a

FIGURE 23b

FIGURE 24

scFv1:A4
scFv2:B4
scFv3:A9
scFv4:C3
scFv5:C9
scFv6:C10
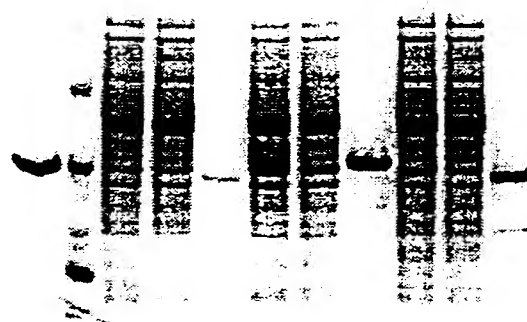scFv7:A10
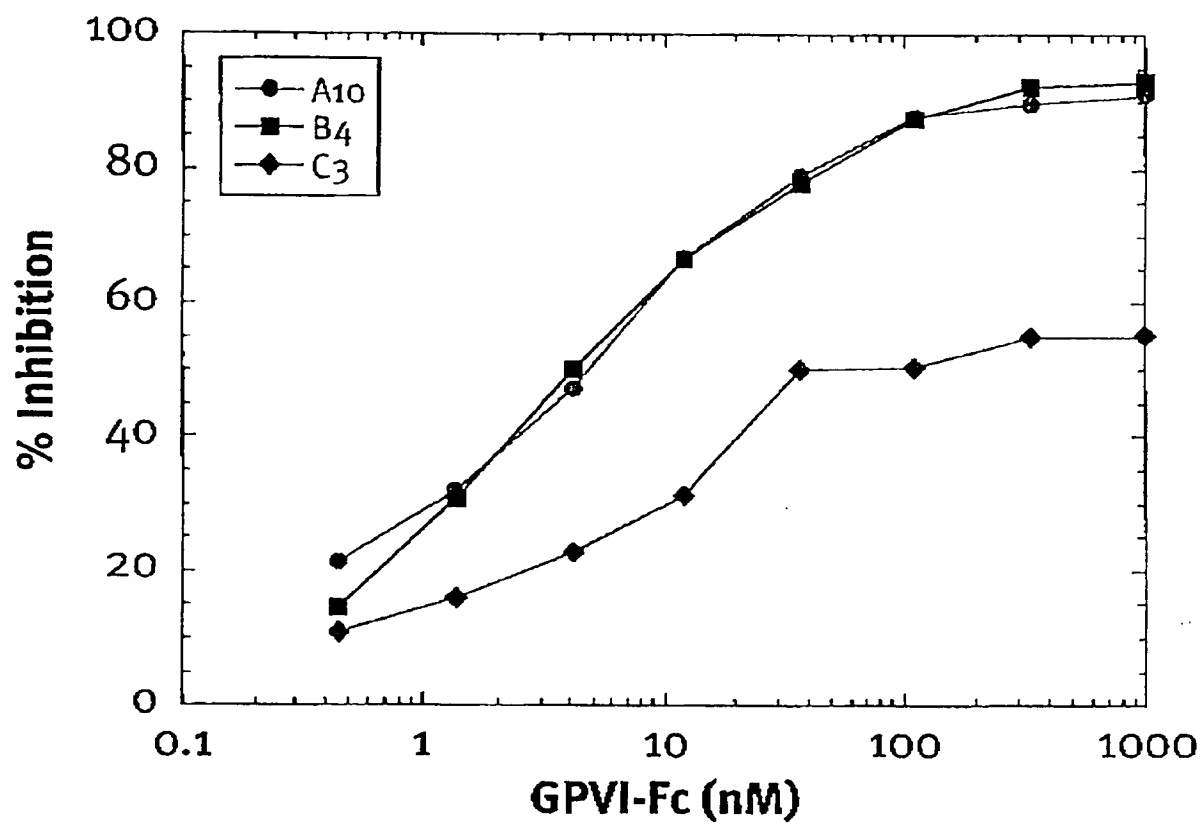
FIGURE 25

A4　　A9　　A10　　　　B4　　C3　　C9　　C10

FIGURE 26

FIGURE 27